

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/882,694A

DATE: 12/21/2001

TIME: 15:29:01

Input Set : N:\Crf3\RULE60\09882694A.txt

Output Set: N:\CRF3\12212001\I882694A.raw

RECEIVED
JAN 08 2002
TECH CENTER 160012900

ENTERED

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5 <110> APPLICANT: Duvick, Jon
7   Maddox, Joyce
9   Gilliam, Jacob
11  Folkerts, Otto
13  Crasta, Oswald R.
17 <120> TITLE OF INVENTION: Compositions and Methods for Fumonisin
19  Detoxification
23 <130> FILE REFERENCE: 5718-111
25 <140> CURRENT APPLICATION NUMBER: 09/882,694A
27 <141> CURRENT FILING DATE: 2001-06-15
30 <150> PRIOR APPLICATION NUMBER: 09/351,224
32 <151> PRIOR FILING DATE: 1999-07-12
36 <160> NUMBER OF SEQ ID NOS: 11
40 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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46 <211> LENGTH: 1691
48 <212> TYPE: DNA
50 <213> ORGANISM: Exophiala spinifera
54 <220> FEATURE:
56 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (0)...(0)
60 <223> OTHER INFORMATION: flavin monooxygenase with intron
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70 aaaatcttcg agggagcccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
72 gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaaat atggaaagac 240
74 tggacctggt cttgccgcta tcttgaccag aaagagttgc tgtcatatgt tcaccactgt 300
76 gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
78 tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
80 aagtatctca ttctcgtac ggggttgctc cacaggaagc aactcccgcc actcccgcc 480
82 ctgcgcgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
84 gagggccaga gattcgccgt catcggtgcc ggggccacaa gcatccagat tgttcaggag 600
86 ttggccaaga aggtgacca ggttaacctg tttatgcgaa ggccgagcta ttgtctgccc 660
88 atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctacccacg 720
90 ctgtttgaag cgagtcgaaa gtctcggatt ggattcccg tccaggcacc gtcggttggc 780
92 atctttgaag tcagcccgga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
94 gcctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
96 ctgggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
98 gatctcatgg ctctctgga gccgcgtac tggttcggta ccaagcgctc cccactggag 1020
100 agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
102 ccattgttgg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggagtc 1140
104 gacacgatcg tgctggcgac ggggttcgac agtttccactg gctcgtgagt gtgctcgatc 1200
106 atggctccga gtcgggacgt ttggctgacc ttgaaagatt gacacatatg ggcttgaaaa 1260
108 acaagcacgg agtggacctg aaggaggtgt ggaaagatgg catatctact tatatgggag 1320
110 tcttctctca tggcttcccc aatgccttct tcgtcgccac ggctcaagcc ccgaccgtcc 1380
112 ttccaacgg cccaacgatc atagaaaccc aagtcgactt gatcgccgat acaattgcaa 1440

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114 agttggaggc cgagcacgcc acgtccgttg aggcgacgaa atcagcacia gaggcattgt 1500
 116 cgattatgat tgccaagatg aacgagcaca ctctgttccc cttgacggat tcgtggtgga 1560
 118 ctggaggcaa catccctggg aaagcaacac gtgctttaac cttcataggc gggattgtc 1620
 120 tctatgagca gatctgtcaa gagaaggtgg ccaattggga tgggtttgat gtgcttcatt 1680
 122 ctccctgcta a 1691

126 <210> SEQ ID NO: 2

128 <211> LENGTH: 1638

130 <212> TYPE: DNA

132 <213> ORGANISM: Exophiala spinifera

136 <220> FEATURE:

138 <221> NAME/KEY: misc_feature

140 <222> LOCATION: (0)...(0)

142 <223> OTHER INFORMATION: flavin monooxygenase, fully spliced

146 <400> SEQUENCE: 2

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 152 aaaatcttcg agggagcccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
 154 gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
 156 tggacctggt cttgccgcta tcctgaccag aaagagttgc tgcataatgt tcaccactgt 300
 158 gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
 160 tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
 162 aagtatctca ttctcgtac ggggttgtc cacaggaagc acactccgc actccccgc 480
 164 ctgcgcgatt tcaacgggaa ggtgatctc tcgagtgcct ggcaagaaga cttcgacgca 540
 166 gagggccaga gactcgcgt catcggtgcc ggggccacaa gcataccagat tgttcaggag 600
 168 ttggccaaga aggtgacca ggtaaccatg tttatgcgaa ggccgagcta ttgtctgccc 660
 170 atggggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctacccacg 720
 172 ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
 174 atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
 176 gcctttaatt ttcttgcttg ccagtaccga gaagtcatgg ttgacaaaaa ggccaaccga 900
 178 ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
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 182 agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
 184 cccattgttg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggaatgc 1140
 186 gacacgatcg tgctggcgac gggtttcgac agtttcaactg gctcattgac acatatgggc 1200
 188 ttgaaaaaca agcacggagt ggacctgaag gaggtgtgga aagatggcat atctacttat 1260
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 192 accgtccttt ccaacggccc aacgatcata gaaacccaag tcgacttgat cgccgataca 1380
 194 attgcaaagt tggaggccga gcacgccacg tccgttgagg cgacgaaatc agcacaagag 1440
 196 gcatggtcga ttatgattgc caagatgaac gagcacactc tgttcccctt gacggattcg 1500
 198 tgggtgactg gaggcaacat cctgggaaa gcaacacgtg ctttaacctt cataggcggg 1560
 200 attgctctct atgagcagat ctgtcaagag aaggtggcca attgggatgg gtttgatgtg 1620
 202 cttcatgctc cctgctaa 1638

206 <210> SEQ ID NO: 3

208 <211> LENGTH: 545

210 <212> TYPE: PRT

212 <213> ORGANISM: Exophiala spinifera

216 <400> SEQUENCE: 3

218 Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp

220 1

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222 Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
224      20      25      30
226 Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
228      35      40      45
230 Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
232      50      55      60
234 Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
236 65      70      75      80
238 Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
240      85      90      95
242 Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
244      100     105     110
246 Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
248      115     120     125
250 Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
252      130     135     140
254 Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
256 145     150     155     160
258 Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
260      165     170     175
262 Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
264      180     185     190
266 Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
268      195     200     205
270 Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
272      210     215     220
274 Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
276 225     230     235     240
278 Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
280      245     250     255
282 Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
284      260     265     270
286 Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
288      275     280     285
290 Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
292      290     295     300
294 Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
296 305     310     315     320
298 Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
300      325     330     335
302 Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
304      340     345     350
306 Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
308      355     360     365
310 Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
312      370     375     380
314 Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
316 385     390     395     400
318 Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly

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320           : 405           410           415
322 Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
324           420           425           430
326 Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr
328           435           440           445
330 Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu
332           450           455           460
334 Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
336 465           470           475           480
338 Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
340           485           490           495
342 Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
344           500           505           510
346 Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
348           515           520           525
350 Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro
352           530           535           540
354 Cys
356 545
362 <210> SEQ ID NO: 4
364 <211> LENGTH: 1464
366 <212> TYPE: DNA
368 <213> ORGANISM: Exophiala spinifera
372 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
376 <222> LOCATION: (0)...(0)
378 <223> OTHER INFORMATION: aldehyde dehydrogenase, fully spliced cDNA
382 <400> SEQUENCE: 4
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388 gatgttcacg tggccaacgc ggccgatgtc gacagtgcag tagccgcttc ggtgcaggcg 180
390 gtcaaaaagg gcccatggaa gaagttcaca ggtgcacaac gcgcggcggtg catgcttaag 240
392 ttgcgcggacc tcgccgagaa gaacgcgcgag aagctcgctc gtctggagtc gctgccacc 300
394 ggtagaccgg tgtcgatgat cactcatttc gacattccaa acatgggtctc cgtgtttcgc 360
396 tactatgcag gctggggccga caagatcgcc ggaaagacct ttcccaggga caacggcaag 420
398 ccgaattggc gttacgagcc gatgggggtg tgtgctggtg ttgccagctg gaacgcgact 480
400 tttcttttacg tcggctggaa gatagccccc gccctcgccg ccggtctgctc ctccatcttc 540
402 aaagcctcgg agaaatcccc gctgggcgtt ctgggcctcg ctccctctct cgcagaagcc 600
404 ggattccctc ctggagtcgt gcagttcctc actggagcac gactgacggg tgaagcattg 660
406 gcgtcgcaca tggacattgc gaagatcagc ttcacaagat ctgtcggcgg tggccgcgcc 720
408 gtcaagcaag caacactcaa gtccaacatg aagcgcgtca ctctagaact gggggaaaag 780
410 ccaaccatcg tottcaacga agtccctctc gaacggcagt cgggggaatc ggcaaaggat 840
412 ttctcaaaat tcgggcaaat ttgggtcccc cctcctgtt tgctagtgca atggggaaat 900
414 ttagcggaga aattccatgg agtccgtcat ggctcatttg gaggtgtca gagatggctt 960
416 ggccagaacc cattggaacc caagaggacg catggtccct tcgtcgacaa gtcccagtac 1020
418 gacagagtct tgggtaacat tgacgttggc aaggataccg cgcagctcct cactggcggt 1080
420 ggtagaaagg gcgacaaggg attcgcgatt gaaccgacga tatttgtcaa tcccaaacca 1140
422 ggcagcaaaa tttggtttga ggagatcttt ggcccgtct tgtccattaa gacgttcaag 1200
424 acggaagaag aggccattga gattgccaat gacacgactt atgggctagc ctcggtcatt 1260

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426 tataccaaat ctctcaacag gggctctccgt gtctcgtcgg cgctcgagac cgggtggcgtc 1320
428 tcgatcaact tcccctttat ccccagagaca caaactccgt ttggcggcat gaaacaatcg 1380
430 ggctcaggca gagagctagg cgaagaaggg ctcaaggcgt acttgagacc caagaccatt 1440
432 aatatccacg tcaacataga gtga 1464
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438 <211> LENGTH: 487
440 <212> TYPE: PRT
442 <213> ORGANISM: Exophiala spinifera
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454 20 25 30
456 Trp Asp Glu Ser Thr Val Ala Thr Asp Val His Val Ala Asn Ala Ala
458 35 40 45
460 Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly
462 50 55 60
464 Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys
466 65 70 75 80
468 Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu
470 85 90 95
472 Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile
474 100 105 110
476 Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys
478 115 120 125
480 Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg
482 130 135 140
484 Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr
486 145 150 155 160
488 Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys
490 165 170 175
492 Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly
494 180 185 190
496 Leu Ala Pro Leu Phe Ala Glu Ala Gly Phe Pro Pro Gly Val Val Gln
498 195 200 205
500 Phe Leu Thr Gly Ala Arg Val Thr Gly Glu Ala Leu Ala Ser His Met
502 210 215 220
504 Asp Ile Ala Lys Ile Ser Phe Thr Arg Ser Val Gly Gly Gly Arg Ala
506 225 230 235 240
508 Val Lys Gln Ala Thr Leu Lys Ser Asn Met Lys Arg Val Thr Leu Glu
510 245 250 255
512 Leu Gly Glu Lys Pro Thr Ile Val Phe Asn Glu Ala Pro Leu Glu Arg
514 260 265 270
516 Gln Ser Gly Glu Ser Ala Lys Asp Phe Ser Lys Phe Gly Gln Ile Trp
518 275 280 285
520 Val Pro Pro Ser Cys Leu Leu Val Gln Trp Gly Asn Leu Ala Glu Lys
522 290 295 300
524 Phe His Gly Val Arg His Gly Ser Phe Gly Gly Cys Gln Arg Trp Leu
526 305 310 315 320

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09882694A.txt

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L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11